

**Amendments to the Specification**

Please replace the paragraph at page 15, lines 25 through 29 with the following amended paragraph:

Based on the above methods, two-dimensional electrophoresis has already been performed for many proteomes. The analytical results obtained by amino acid sequencing and peptide mass fingerprinting methods performed on isolated protein spots have been ~~recorded along~~ recorded along with coordinate information, and stored in databases such as SWISS-2DPAGE® (~~<http://expasy.heuge.ch/ch2d/>~~), etc.

Please replace the paragraph at page 24, lines 4 through 12 with the following amended paragraph:

On the other hand, compared with labor-intensive amino acid sequencing, peptide mass-fingerprinting methods can more speedily provide a variety of information useful for protein identification. Mass patterns (i.e. fingerprints) of the protease-digested fragments are obtained by using a set protease to digest the proteins contained in the spots separated as a result of two-dimensional electrophoresis, and then analyzing the fragments thus obtained using a mass spectrogram. Proteins can be identified based on these peptide mass fingerprints since they are information highly unique to individual proteins, and databases which accumulate such data, such as ~~ProteinProspector~~ PROTEINPROSPECTOR® (~~<http://prospector.ucsf.edu/>~~), can be utilized on the Internet.